

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/755,320
Source: IFW16
Date Processed by STIC: 01/26/2006

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 01/26/2006
PATENT APPLICATION: US/09/755,320 **TIME:** 10:10:26

Input Set : N:\Crf3\RULE60\09755320.raw.txt
Output Set: N:\CRF4\01262006\I755320.raw

SEQUENCE LISTING

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PATENT APPLICATION: US/09/755,320

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| | | | | | | | |
|-----|----------------------------|---------------|-----------------|-----------------|-------------|-----------------------------|---------|
| 63 | (A) NAME/KEY: | CDS | | | | | |
| 64 | (B) LOCATION: | 197..1108 | | | | | |
| 67 | (xi) SEQUENCE DESCRIPTION: | SEQ ID NO: 1: | | | | | |
| 69 | GTCAAGTGTT | TATACTGCA | GGAGACTGGC | CGCTCGGCTC | AGGACTGGGA | TTAGCGGGCT | 60 |
| 71 | CTGCTAAAC | CCGCGGGCT | TTTACATTAG | GAGTGAGTGG | GGGAGAGTCC | TAGGATTCT | 120 |
| 73 | AGTGAAAAGT | GACAGCGCTT | GGTGGACTTT | GGGACCTTCG | TGAAGTCTTC | TGCTTGGAAAG | 180 |
| 75 | CTGAGACTTG | CATGCC | ATG GAA | CAC CCC | CTC TTT | GGC TGC CTG CGC AGC | 229 |
| 76 | | | Met Glu His Pro | Leu Phe Gly Cys | Leu Arg Ser | | |
| 77 | 1 | | 5 | | 10 | | |
| 79 | CCC CAC | GCC ACA | GCG CAA | GGC TTG | CAC CCC | TTC TCG CAG TCT | 277 |
| 80 | Pro His | Ala Thr | Ala Gln | Gly Leu | His Pro | Phe Ser Gln Ser Ser | Leu |
| 81 | 15 | | 20 | | 25 | | |
| 83 | GCC CTC | CAT GGA | AGA TCT | GAC CAC | ATG TCC | TAC CCC GAA | 325 |
| 84 | Ala Leu | His Gly | Arg Ser Asp | His Met | Ser Tyr | Pro Glu Leu Ser Thr | |
| 85 | 30 | | 35 | | 40 | | |
| 87 | TCT TCC | TCG TCT | TGC ATA | ATC GCG | GGA TAC | CCC AAT GAG | 373 |
| 88 | Ser Ser | Ser Ser | Cys Ile | Ile Ala | Gly Tyr | Pro Asn Glu Glu Gly | Met |
| 89 | 45 | | 50 | | 55 | | |
| 91 | TTT GCC | AGC CAG | CAT CAC | AGG GGG | CAC CAC | CAC CAC CAC CAC | 421 |
| 92 | Phe Ala | Ser Gln | His His | Arg Gly | His His | His His His His His | |
| 93 | 60 | | 65 | | 70 | | 75 |
| 95 | CAT CAC | CAC CAC | CAG CAG | CAG CAG | CAC CAG | GCT CTG CAA AGC AAC | 469 |
| 96 | His His | His His | Gln Gln | Gln Gln | His Gln | Ala Leu Gln Ser Asn Trp | |
| 97 | 80 | | 85 | | 90 | | |
| 99 | CAC CTC | CCG CAG | ATG TCC | TCC CCG | CCA AGC | GCG GCC CGG CAC AGC | 517 |
| 100 | His Leu | Pro Gln | Met Ser | Ser Pro | Pro Ser | Ala Ala Arg His Ser | Leu |
| 101 | 95 | | 100 | | 105 | | |
| 103 | TGC CTG | CAG CCT | GAT TCC | GGA GGG | CCC CCG | GAG CTG GGG AGC AGC | 565 |
| 104 | Cys Leu | Gln Pro | Asp Ser | Gly Gly | Pro Pro | Glu Leu Gly Ser Ser | Pro |
| 105 | 110 | | 115 | | 120 | | |
| 107 | CCG GTC | CTG TGC | TCC AAC | TCT TCT | AGC CTG | GGC TCC AGC ACC CCG ACC | 613 |
| 108 | Pro Val | Leu Cys | Ser Asn | Ser Ser | Leu Gly | Ser Ser Thr Pro Thr | |
| 109 | 125 | | 130 | | 135 | | |
| 111 | GGA GCG | TGC GCA | CCA AGG | GAT TAT | GGC CGT | CAA GCG CTG TCA CCC | 661 |
| 112 | Gly Ala | Ala Cys | Ala Pro | Arg Asp | Tyr Gly | Arg Gln Ala Leu Ser | Pro |
| 113 | 140 | | 145 | | 150 | | 155 |
| 115 | GCA GAA | GTG GAG | AAG AGA | AGT GGC | AGC AAA | AGA AAA AGC GAC AGT | 709 |
| 116 | Ala Glu | Val Glu | Lys Arg | Ser Gly | Ser Lys | Arg Lys Ser Asp Ser | Ser |
| 117 | 160 | | 165 | | 170 | | |
| 119 | GAT TCC | CAG GAA | GGAA AAT | TAC AAG | TCA GAA | GTG AAC AGC AGC AAA CCT AGG | 757 |
| 120 | Asp Ser | Gln Glu | Gly Asn | Tyr Lys | Ser Glu | Val Asn Ser Lys | Pro Arg |
| 121 | 175 | | 180 | | 185 | | |
| 123 | AGG GAA | AGA ACA | GCT TTC | ACC AAA | GAG CAA | ATC AGA GAA CTT GAG GCA | 805 |
| 124 | Arg Glu | Arg Thr | Ala Phe | Thr Lys | Glu Gln | Ile Arg Glu Leu Glu | Ala |
| 125 | 190 | | 195 | | 200 | | |
| 127 | GAG TTC | GCC CAT | CAT AAC | TAT CTG | ACC AGA | CTG AGA AGA TAT GAG | 853 |
| 128 | Glu Phe | Ala His | His Asn | Tyr Leu | Thr Arg | Leu Arg Arg Tyr Glu | Ile |
| 129 | 205 | | 210 | | 215 | | |
| 131 | GCG GTG | AAC CTA | GAC CTC | ACT GAA | AGA CAG | GTG AAA GTG TGG TTC CAG | 901 |

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| | | | | | | | | | | | | | | | | |
|-----|------------|-------------------------------------|-------------|------------|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|
| 132 | Ala | Val | Asn | Leu | Asp | Leu | Thr | Glu | Arg | Gln | Val | Lys | Val | Trp | Phe | Gln |
| 133 | 220 | | | | | 225 | | | | | 230 | | | | | 235 |
| 135 | AAC | AGG | AGA | ATG | AAG | TGG | AAG | CGG | GTC | AAG | GGG | GGA | CAA | CAA | GGA | GCT |
| 136 | Asn | Arg | Arg | Met | Lys | Trp | Lys | Arg | Val | Lys | Gly | Gly | Gln | Gln | Gly | Ala |
| 137 | | | | | | 240 | | | | 245 | | | | | 250 | |
| 139 | GCA | GCC | CGA | GAA | AAG | GAA | CTG | GTG | AAT | GTG | AAA | AAG | GGA | ACA | CTT | CTT |
| 140 | Ala | Ala | Arg | Glu | Lys | Glu | Leu | Val | Asn | Val | Lys | Lys | Gly | Thr | Leu | Leu |
| 141 | | | | | | 255 | | | 260 | | | | | 265 | | |
| 143 | CCA | TCA | GAG | CTG | TCA | GGA | ATT | GGT | GCA | GCC | ACC | CTC | CAG | CAG | ACA | GGG |
| 144 | Pro | Ser | Glu | Leu | Ser | Gly | Ile | Gly | Ala | Ala | Thr | Leu | Gln | Gln | Thr | Gly |
| 145 | | | | | | 270 | | | 275 | | | | | 280 | | |
| 147 | GAC | TCA | CTA | GCA | AAT | GAC | GAC | AGT | CGC | GAT | AGT | GAC | CAC | AGC | TCT | GAG |
| 148 | Asp | Ser | Leu | Ala | Asn | Asp | Asp | Ser | Arg | Asp | Ser | Asp | His | Ser | Ser | Glu |
| 149 | | | | | | 285 | | | 290 | | | | 295 | | | |
| 151 | CAC | GCA | CAC | TTA | TGATACATAC | AGAGACCAGC | TCCGTTCTCA | GGAAAGCACC | | | | | | | | |
| 152 | His | Ala | His | Leu | | | | | | | | | | | | |
| 153 | 300 | | | | | | | | | | | | | | | |
| 155 | ATTGTGATGG | CAAATCTCAC | CCAAACATCG | TTTACATGGC | AGATGACTGT | GGCAGTGTG | | | | | | | | | | |
| 157 | CTTAATATAA | TTAACCGCAG | GCATCTCAAG | TCTGTTCTC | ATGATTGATA | GAAGGTTTAC | | | | | | | | | | |
| 159 | ACTAAGTGCC | TCTTATTGAA | GATGCTTCCA | CAGTGAAATT | GGAGAAAGTG | AACATATCTA | | | | | | | | | | |
| 161 | AATATACTTG | TTCCTTATAT | GACAGAGAGG | GAGATGAATG | TTTGCTTGG | CTTGCACTGA | | | | | | | | | | |
| 163 | AAATTAAATT | GCTACCAAGA | GCAAACCTCGG | TAAGACATT | TGACTCAAGT | TGTCCTCCAGA | | | | | | | | | | |
| 165 | GTGAAGATGT | TATAGAAATG | CTTGAAACAT | TCCAGTTGTA | CCAGGTATG | TGTGTGACAC | | | | | | | | | | |
| 167 | TGGGCAGGTA | TTTGCTTTG | CTTGCACGTGA | AACTAAACT | GCTATCAAGT | TAACCCATGA | | | | | | | | | | |
| 169 | AATAGTTAT | CTTGAACAGC | CACAGTGCCT | GAAATCACCA | AGTGGATATA | AAATGAAC | | | | | | | | | | |
| 171 | AAATTCTGTA | TATATTACTC | CTAACGTATT | TTCCTGTCTT | CACTAATT | AGCAAATGCA | | | | | | | | | | |
| 173 | TTCATATTAG | CTGATGAAAA | TAGGCTTCC | CGTGGACAAA | TGCAGCCAGC | TTCTTGATT | | | | | | | | | | |
| 175 | TTTATACATT | TTTTTGTCA | TCAGAGACAT | CAGTATGTGC | TTACTTGTTG | TCAAGTAGAG | | | | | | | | | | |
| 177 | GAAATGCAGT | AGAGTCTGAT | AGGACATATT | CTTGGTACCA | CAGACAAAAC | AAATCTTCTG | | | | | | | | | | |
| 179 | TTGCATTGAC | TATCAACTGC | TGCAGATACA | TTAGAGAAC | CACCTAGCCC | CCCTCCAGCC | | | | | | | | | | |
| 181 | TCCCTCTGTT | ATCGCTCGAA | GACATTAGCG | TCATAGGCAA | GTAGTTACCT | TGCCAAATGA | | | | | | | | | | |
| 183 | GTCTTGTGT | GCAGATGTCT | GATTTGTAT | CTTTAAACTG | TTAATGGTAT | GTGTCTGCTT | | | | | | | | | | |
| 185 | CAGTTAACAG | GGAAAAAGAT | TTCTTCCTCA | TTGTTTATGA | TACAAAACCC | AAGTGCCAAA | | | | | | | | | | |
| 187 | CAAAGCTAGT | TCTTCAGGG | ATAGATGAGA | AACTGAATGT | CTGACAAGTA | GACTCAGCGA | | | | | | | | | | |
| 189 | AAATACATTA | TTTTTCAGAG | GCTGTGTATT | CATGCAGTAC | AAGTCCTTGT | ATTGGTAAA | | | | | | | | | | |
| 191 | AAAAAAAGTT | AAATAAATG | | | | | | | | | | | | | | |
| 194 | (2) | INFORMATION FOR SEQ ID NO: 2: | | | | | | | | | | | | | | |
| 196 | (i) | SEQUENCE CHARACTERISTICS: | | | | | | | | | | | | | | |
| 197 | (A) | LENGTH: 303 amino acids | | | | | | | | | | | | | | |
| 198 | (B) | TYPE: amino acid | | | | | | | | | | | | | | |
| 199 | (D) | TOPOLOGY: linear | | | | | | | | | | | | | | |
| 201 | (ii) | MOLECULE TYPE: protein | | | | | | | | | | | | | | |
| 203 | (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 2: | | | | | | | | | | | | | | |
| 205 | Met | Glu | His | Pro | Leu | Phe | Gly | Cys | Leu | Arg | Ser | Pro | His | Ala | Thr | Ala |
| 206 | 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| 208 | Gln | Gly | Leu | His | Pro | Phe | Ser | Gln | Ser | Ser | Leu | Ala | Leu | His | Gly | Arg |
| 209 | | | | | | 20 | | | 25 | | | | | 30 | | |
| 211 | Ser | Asp | His | Met | Ser | Tyr | Pro | Glu | Leu | Ser | Thr | Ser | Ser | Ser | Ser | Cys |
| 212 | | | | | | 35 | | | 40 | | | | | 45 | | |

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214 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His
215 50 55 60
217 His Arg Gly His Gln
218 65 70 75 80
220 Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His Leu Pro Gln Met
221 85 90 95
223 Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp
224 100 105 110
226 Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser
227 115 120 125
229 Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala
230 130 135 140
232 Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Val Glu Lys
233 145 150 155 160
235 Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly
236 165 170 175
238 Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Arg Glu Arg Thr Ala
239 180 185 190
241 Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His
242 195 200 205
244 Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp
245 210 215 220
247 Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys
248 225 230 235 240
250 Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys
251 245 250 255
253 Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser
254 260 265 270
256 Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp Ser Leu Ala Asn
257 275 280 285
259 Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His Ala His Leu
260 290 295 300

263 (2) INFORMATION FOR SEQ ID NO: 3:

265 (i) SEQUENCE CHARACTERISTICS:
266 (A) LENGTH: 941 base pairs
267 (B) TYPE: nucleic acid
268 (C) STRANDEDNESS: both
269 (D) TOPOLOGY: linear

271 (ii) MOLECULE TYPE: cDNA

273 (iii) HYPOTHETICAL: NO

275 (iv) ANTI-SENSE: NO

278 (ix) FEATURE:

279 (A) NAME/KEY: CDS

280 (B) LOCATION: 33..941

283 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

285 GTCTTCTACC TGGAACCGA AACTTGCATG CT ATG GAA CAC CCG CTC TTT GGC
286 Met Glu His Pro Leu Phe Gly
287 1 5
289 TGC CTG CGC AGC CCT CAC GCC ACG GCG CAA GGC TTG CAC CCG TTC TCC

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 290 | Cys | Leu | Arg | Ser | Pro | His | Ala | Thr | Ala | Gln | Gly | Leu | His | Pro | Phe | Ser |
| 291 | 10 | | | | 15 | | | | | | | 20 | | | | |
| 293 | CAA | TCC | TCT | CTC | GCC | CTC | CAT | GGA | AGA | TCT | GAC | CAT | ATG | TCT | TAC | CCC |
| 294 | Gln | Ser | Ser | Leu | Ala | Leu | His | Gly | Arg | Ser | Asp | His | Met | Ser | Tyr | Pro |
| 295 | 25 | | | | 30 | | | | | | 35 | | | | | |
| 297 | GAG | CTC | TCT | ACT | TCT | TCC | TCA | TCT | TGC | ATA | ATC | GCG | GGA | TAC | CCC | AAC |
| 298 | Glu | Leu | Ser | Thr | Ser | Ser | Ser | Ser | Cys | Ile | Ile | Ala | Gly | Tyr | Pro | Asn |
| 299 | 40 | | | | 45 | | | | | 50 | | | 55 | | | |
| 301 | GAA | GAG | GAC | ATG | TTT | GCC | AGC | CAG | CAT | CAC | AGG | GGG | CAC | CAC | CAC | CAC |
| 302 | Glu | Glu | Asp | Met | Phe | Ala | Ser | Gln | His | His | Arg | Gly | His | His | His | His |
| 303 | | | | | 60 | | | | | 65 | | | 70 | | | |
| 305 | CAC | CAC | CAC | CAT | CAC | CAC | CAT | CAG | CAG | CAG | CAC | CAG | GCT | CTG | CAA | |
| 306 | His | Gln | Gln | Gln | Gln | Gln | His | Gln | Ala | Leu |
| 307 | | | | | 75 | | | | 80 | | | 85 | | | | |
| 309 | ACC | AAC | TGG | CAC | CTC | CCG | CAG | ATG | TCT | TCC | CCA | CCG | AGT | GCG | GCT | CGG |
| 310 | Thr | Asn | Trp | His | Leu | Pro | Gln | Met | Ser | Ser | Pro | Pro | Ser | Ala | Ala | Arg |
| 311 | | | | | 90 | | | | 95 | | | 100 | | | | |
| 313 | CAT | AGC | CTC | TGC | CTC | CAG | CCC | GAC | TCT | GGA | GGG | CCC | CCA | GAG | TTG | GGG |
| 314 | His | Ser | Leu | Cys | Leu | Gln | Pro | Asp | Ser | Gly | Gly | Pro | Pro | Glu | Leu | Gly |
| 315 | | | | | 105 | | | | 110 | | | 115 | | | | |
| 317 | AGC | AGC | CCG | CCC | GTC | CTG | TGC | TCC | AAC | TCT | TCC | AGC | TTG | GGC | TCC | AGC |
| 318 | Ser | Ser | Pro | Pro | Val | Leu | Cys | Ser | Asn | Ser | Ser | Leu | Gly | Ser | Ser | |
| 319 | 120 | | | | 125 | | | | | 130 | | | 135 | | | |
| 321 | ACC | CCG | ACT | GGG | GCC | GCG | TGC | GCG | CCG | GGG | GAC | TAC | GGC | CGC | CAG | GCA |
| 322 | Thr | Pro | Thr | Gly | Ala | Ala | Cys | Ala | Pro | Gly | Asp | Tyr | Gly | Arg | Gln | Ala |
| 323 | | | | | 140 | | | | 145 | | | 150 | | | | |
| 325 | CTG | TCA | CCT | GCG | GAG | GCG | GAG | AAG | CGA | AGC | GGC | GGC | AAG | AGG | AAA | AGC |
| 326 | Leu | Ser | Pro | Ala | Glu | Ala | Glu | Lys | Arg | Ser | Gly | Gly | Lys | Arg | Lys | Ser |
| 327 | | | | | 155 | | | | 160 | | | 165 | | | | |
| 329 | GAC | AGC | TCA | GAC | TCC | CAG | GAA | GGA | AAT | TAC | AAG | TCA | GAA | GTC | AAC | AGC |
| 330 | Asp | Ser | Ser | Asp | Ser | Gln | Glu | Gly | Asn | Tyr | Lys | Ser | Glu | Val | Asn | Ser |
| 331 | | | | | 170 | | | | 175 | | | 180 | | | | |
| 333 | AAA | CCC | AGG | AAA | GAA | AGG | ACA | GCA | TTT | ACC | AAA | GAG | CAA | ATC | AGA | GAA |
| 334 | Lys | Pro | Arg | Lys | Glu | Arg | Thr | Ala | Phe | Thr | Lys | Glu | Gln | Ile | Arg | Glu |
| 335 | | | | | 185 | | | | 190 | | | 195 | | | | |
| 337 | CTT | GAA | GCA | GAA | TTT | GCC | CAT | CAT | AAT | TAT | CTC | ACC | AGA | CTG | AGG | CGA |
| 338 | Leu | Glu | Ala | Glu | Phe | Ala | His | His | Asn | Tyr | Leu | Thr | Arg | Leu | Arg | Arg |
| 339 | 200 | | | | 205 | | | | | 210 | | | 215 | | | |
| 341 | TAC | GAG | ATA | GCA | GTG | AAT | CTG | GAT | CTC | ACT | GAA | AGA | CAG | GTA | AAA | GTC |
| 342 | Tyr | Glu | Ile | Ala | Val | Asn | Leu | Asp | Leu | Thr | Glu | Arg | Gln | Val | Lys | Val |
| 343 | | | | | 220 | | | | 225 | | | 230 | | | | |
| 345 | TGG | TTC | CAA | AAC | AGG | CGG | ATG | AAG | TGG | AAG | AGG | GTA | AAG | GGT | GGA | CAG |
| 346 | Trp | Phe | Gln | Asn | Arg | Arg | Met | Lys | Trp | Lys | Arg | Val | Lys | Gly | Gly | Gln |
| 347 | | | | | 235 | | | | 240 | | | 245 | | | | |
| 349 | CAA | GGA | GCT | GCG | GCT | CGG | GAA | AAG | GAA | CTG | GTG | AAT | GTG | AAA | AAG | GGA |
| 350 | Gln | Gly | Ala | Ala | Ala | Arg | Glu | Lys | Glu | Leu | Val | Asn | Val | Lys | Lys | Gly |
| 351 | | | | | 250 | | | | 255 | | | 260 | | | | |
| 353 | ACA | CTT | CTC | CCA | TCA | GAG | CTG | TCG | GGA | ATT | GGT | GCA | GCC | ACC | CTC | CAG |
| 354 | Thr | Leu | Leu | Pro | Ser | Glu | Leu | Ser | Gly | Ile | Gly | Ala | Ala | Thr | Leu | Gln |

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:34 M:238 W: Alpha Fields not Ordered [(C) CLASSIFICATION:] of (1) (vi)